

SEQUENCE LISTING

<110> Fox, Brian A.
Gao, Zeren
Shoemaker, Kimberly E.

<120> NEUROPILIN HOMOLOG ZCUB5

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<151> 2000-11-15

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Met Val Pro Gly Ala Arg Gly Gly Gly Ala Leu Ala

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cgg gct gcc ggg cggtt gct ttg ctg ctc gcg gtc tcc gcc 159
Arg Ala Ala Gly Arg Gly Leu Leu Ala Leu Leu Ala Val Ser Ala
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ccg ctc cgg ctg cag gcg gag gag ctg ggt gat ggc tgt gga cac cta 207
Pro Leu Arg Leu Gln Ala Glu Glu Leu Gly Asp Gly Cys Gly His Leu
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acc tgt gct tct gac tat ctt ctc ttc acc agc tct tca gat caa tat Thr Cys Ala Ser Asp Tyr Leu Leu Phe Thr Ser Ser Asp Gln Tyr 95 100 105	399
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aca tgt ttg gaa cga gct agc cat tat ttg aag aca gaa tac agc aaa Thr Cys Leu Glu Arg Ala Ser His Tyr Leu Lys Thr Glu Tyr Ser Lys 160 165 170	591
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His Thr Val Cys Glu Lys Thr Ile Thr Val Pro Lys Gly Lys Arg Leu			
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Ile Leu Arg Leu Gly Asp Leu Asp Ile Glu Ser Gln Thr Cys Ala Ser			
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Gly Ser Met Thr Val Pro Lys Glu Leu Leu Leu Asn Thr Ser Glu Val			
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Thr Val Arg Phe Glu Ser Gly Ser His Ile Ser Gly Arg Gly Phe Leu			
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Arg Ala Ser His Tyr Leu Lys Thr Glu Tyr Ser Lys Phe Cys Pro Ala			
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 Tyr Arg Asp Thr Ser Leu Leu Cys Lys Ala Ala Ile His Ala Gly Ile
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 Arg Ser Leu Ser Phe Glu Pro Asp Gly Gln Ile Arg Ala Ser Ser Ser
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 Gln Ala Arg Leu Gln Asp Gln Gly Pro Ser Trp Ala Ser Gly Asp Ser
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 Ser Asn Asn His Lys Pro Arg Glu Trp Leu Glu Ile Asp Leu Gly Glu
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 Lys Lys Lys Ile Thr Gly Ile Arg Thr Thr Gly Ser Thr Gln Ser Asn
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 Ser Lys Trp Lys Thr Tyr Lys Gly Ile Val Asn Asn Glu Glu Lys Val
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 Gly Asn Asp Ser Leu Val Trp Arg Lys Thr Ser Gln Ser Thr Ser Val
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 Arg Lys Lys Lys Lys Lys Gly Ser Pro Tyr Gly Ser Ala Glu Ala Gln
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 Lys Thr Asp Cys Trp Lys Gln Ile Lys Tyr Pro Phe Ala Arg His Gln
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Ser Ala Glu Phe Thr Ile Ser Tyr Asp Asn Glu Lys Glu Met Thr Gln
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 Met Ile Gly Thr Gly Thr Val Thr Arg Lys Gly Ser Thr Phe Arg Pro
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 His Tyr Asp Cys Pro Gln Arg Ala Gly Arg His Glu Tyr Ala Leu Pro
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 Val Leu Arg Ala His Thr Phe Ser Ala Gln Ser Gly Tyr Arg Val Pro
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 Gly Pro Gln Pro Gly His Lys His Ser Leu Ser Ser Gly Gly Phe Ser
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 Pro Val Ala Gly Val Gly Ala Gln Asp Gly Asp Tyr Gln Arg Pro His
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 Ser Ala Gln Pro Ala Asp Arg Gly Tyr Asp Arg Pro Lys Ala Val Ser
 660 665 670
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atc aca gtc cca aag ggg aag aga ctt att ctg agg ttggat Ile Thr Val Pro Lys Gly Lys Arg Leu Ile Leu Arg Leu Gly Asp Leu 65 70 75	362
aac att gag tcc aag acc tgc gct tct gac tat ctc ctc ttc agc agt Asn Ile Glu Ser Lys Thr Cys Ala Ser Asp Tyr Leu Leu Phe Ser Ser 80 85 90	410
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gaa ctc cggttgc aac tca aac gaa gtg act gtc ctc ttc aag agt gga Glu Leu Arg Leu Asn Ser Asn Glu Val Thr Val Leu Phe Lys Ser Gly 115 120 125	506
tct cac att tct ggc cggttgc ttt ctg ctg acc tac gcc agc agt gac Ser His Ile Ser Gly Arg Gly Phe Leu Leu Thr Tyr Ala Ser Ser Asp 130 135 140	554
cat cca gat tta ata acc tgt ttg gaa cga ggc agc cat tat ttc gag His Pro Asp Leu Ile Thr Cys Leu Glu Arg Gly Ser His Tyr Phe Glu 145 150 155	602
gaa aaa tac agc aaa ttc tgc cca gct ggc tgt aga gac ata gca gga Glu Lys Tyr Ser Lys Phe Cys Pro Ala Gly Cys Arg Asp Ile Ala Gly 160 165 170	650
gat att tct ggg aat aca aaa gat ggt tac aga gat acc tct tta ttg Asp Ile Ser Gly Asn Thr Lys Asp Gly Tyr Arg Asp Thr Ser Leu Leu 175 180 185 190	698

POSTER PRESENTED AT THE 1998 AACR MEETING

tgc aaa gct gcc atc cac gca ggg atc atc aca gat gaa cta ggt ggc Cys Lys Ala Ala Ile His Ala Gly Ile Ile Thr Asp Glu Leu Gly Gly	195	200	205	746
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 ctg gcc aat ggc gtg ctc tcc cg ^g cat ggt tct ttg tcg gaa aag cga Leu Ala Asn Gly Val Leu Ser Arg His Gly Ser Leu Ser Glu Lys Arg	225	230	235	842
 ttt ctt ttt aca acc cca gga atg aat att aca act gtg gc ^g att cca Phe Leu Phe Thr Thr Pro Gly Met Asn Ile Thr Thr Val Ala Ile Pro	240	245	250	890
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 atc tgt aga aag agg aaa aag aaa gga aat cca tat gtg tca gct gac Ile Cys Arg Lys Arg Lys Lys Gly Asn Pro Tyr Val Ser Ala Asp	275	280	285	986
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 Tyr Pro Gly Thr Tyr Pro Asn Tyr Thr Val Cys Glu Lys Ile Ile Thr
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 Glu Ser Lys Thr Cys Ala Ser Asp Tyr Leu Leu Phe Ser Ser Ala Thr
 85 90 95
 Asp Gln Tyr Gly Pro Tyr Cys Gly Ser Trp Ala Val Pro Lys Glu Leu
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 Arg Leu Asn Ser Asn Glu Val Thr Val Leu Phe Lys Ser Gly Ser His
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 Ile Ser Gly Arg Gly Phe Leu Leu Thr Tyr Ala Ser Ser Asp His Pro
 130 135 140

Asp Leu Ile Thr Cys Leu Glu Arg Gly Ser His Tyr Phe Glu Glu Lys
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 Tyr Ser Lys Phe Cys Pro Ala Gly Cys Arg Asp Ile Ala Gly Asp Ile
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 Ser Gly Asn Thr Lys Asp Gly Tyr Arg Asp Thr Ser Leu Leu Cys Lys
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 Ala Ala Ile His Ala Gly Ile Ile Thr Asp Glu Leu Gly Gly His Ile
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 Asn Gly Val Leu Ser Arg His Gly Ser Leu Ser Glu Lys Arg Phe Leu
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 Phe Thr Thr Pro Gly Met Asn Ile Thr Thr Val Ala Ile Pro Ser Val
 245 250 255
 Ile Phe Ile Ala Leu Leu Leu Thr Gly Met Gly Ile Phe Ala Ile Cys
 260 265 270
 Arg Lys Arg Lys Lys Gly Asn Pro Tyr Val Ser Ala Asp Ala Gln
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 Lys Thr Gly Cys Trp Lys Gln Ile Lys Tyr Pro Phe Ala Arg His Gln
 290 295 300
 Ser Thr Glu Phe Thr Ile Ser Tyr Asp Asn Glu Lys Glu Met Thr Gln
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 Lys Leu Asp Leu Ile Thr Ser Asp Met Ala Asp Tyr Gln Gln Pro Leu
 325 330 335
 Met Ile Gly Thr Gly Thr Val Ala Arg Lys Gly Ser Thr Phe Arg Pro
 340 345 350
 Met Asp Thr Asp Thr Glu Glu Val Arg Val Asn Thr Glu Ala Ser Gly
 355 360 365
 His Tyr Asp Cys Pro His Arg Pro Gly Arg His Glu Tyr Ala Leu Pro
 370 375 380
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 405 410 415
 Gly Pro Arg Pro Thr His Lys His Ser His Ser Ser Gly Gly Phe Pro
 420 425 430
 Pro Ala Thr Gly Ala Thr Gln Val Glu Ser Tyr Gln Arg Pro Ala Ser
 435 440 445
 Pro Lys Pro Val Gly Gly Tyr Asp Lys Pro Ala Ala Ser Ser Phe
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 Leu Asp Ser Arg Asp Pro Ala Ser Gln Ser Gln Met Thr Ser Gly Gly
 465 470 475 480

Asp Asp Gly Tyr Ser Ala Pro Arg Asn Gly Leu Ala Pro Leu Asn Gln
485 490 495

Thr Ala Met Thr Ala Leu Leu
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ggg gct ggt ggg ccg agt gtc ctg gcg ctg ctg ttc gcc gtg tgt gct
Gly Ala Gly Gly Pro Ser Val Leu Ala Leu Leu Phe Ala Val Cys Ala
5 10 15

ccg ctc cggttg cag gcg gag gag ctgggt gat ggc tgt ggg cac ata
Pro Leu Arg Leu Glu Ala Glu Glu Leu Gly Asp Gly Cys Gly His Ile
20 25 30 35

gtg acc tct cag gac agt ggc aca atg aca tct aag aat tat cca ggg 262
 Val Thr Ser Gln Asp Ser Gly Thr Met Thr Ser Lys Asn Tyr Pro Gly
 40 45 50

act tac ccc aat tac act gtg tgt gaa aag atc atc aca gtc cca aag 310
Thr Tyr Pro Asn Tyr Thr Val Cys Glu Lys Ile Ile Thr Val Pro Lys
55 60 65

ggg aag aga ctt att ctg agg ttg gga gat ttg aac att gag tcc aag 358
Gly Lys Arg Leu Ile Leu Arg Leu Gly Asp Leu Asn Ile Glu Ser Lys
70 75 80

acc tgc gct tct gac tat ctc ctc ttc agc agt gca aca gat cag tat 406
Thr Cys Ala Ser Asp Tyr Leu Leu Phe Ser Ser Ala Thr Asp Gln Tyr
85 90 95

gat tta ata acc tgt ttg gaa cga ggc agc cat tat ttc gag gaa aaa Asp Leu Ile Thr Cys Leu Glu Arg Gly Ser His Tyr Phe Glu Glu Lys 100 105 110 115	454
tac agc aaa ttc tgc cca gct ggc tgt aga gac ata gca gga gat att Tyr Ser Lys Phe Cys Pro Ala Gly Cys Arg Asp Ile Ala Gly Asp Ile 120 125 130	502
tct ggg aat aca aaa gat ggt tac aga gat acc tct tta ttg tgc aaa Ser Gly Asn Thr Lys Asp Gly Tyr Arg Asp Thr Ser Leu Leu Cys Lys 135 140 145	550
gct gcc atc cac gca ggg atc atc aca gat gaa cta ggt ggc cac atc Ala Ala Ile His Ala Gly Ile Ile Thr Asp Glu Leu Gly Gly His Ile 150 155 160	598
aac ttg ctt cag agc aaa ggg ata agt cac tat gaa gga ctc ctg gcc Asn Leu Leu Gln Ser Lys Gly Ile Ser His Tyr Glu Gly Leu Leu Ala 165 170 175	646
aat ggc gtg ctc tcc cgg cat ggt tct ttg tcg gaa aag cga ttt ctt Asn Gly Val Leu Ser Arg His Gly Ser Leu Ser Glu Lys Arg Phe Leu 180 185 190 195	694
ttt aca acc cca gga atg aat att aca act gtg gcg att cca tca gtg Phe Thr Thr Pro Gly Met Asn Ile Thr Thr Val Ala Ile Pro Ser Val 200 205 210	742
atc ttc atc gcc ctc ctt ctg act gga atg ggg atc ttt gca atc tgt Ile Phe Ile Ala Leu Leu Thr Gly Met Gly Ile Phe Ala Ile Cys 215 220 225	790
aga aag agg aaa aag aaa gga aat cca tat gtg tca gct gac gct cag Arg Lys Arg Lys Lys Gly Asn Pro Tyr Val Ser Ala Asp Ala Gln 230 235 240	838
aaa aca ggc tgt tgg aag cag att aaa tat ccc ttt gcc agg cat cag Lys Thr Gly Cys Trp Lys Gln Ile Lys Tyr Pro Phe Ala Arg His Gln 245 250 255	886

tcg acg gaa ttt acc atc agc tat gac aat gaa aaa gag atg aca caa Ser Thr Glu Phe Thr Ile Ser Tyr Asp Asn Glu Lys Glu Met Thr Gln 260 265 270 275	934
aag ttg gat ctc atc act agt gat atg gca gat tat cag cag cct ctc Lys Leu Asp Leu Ile Thr Ser Asp Met Ala Asp Tyr Gln Gln Pro Leu 280 285 290	982
atg att ggc aca ggc aca gtc gcg aga aag ggc tct acc ttc cga ccc Met Ile Gly Thr Gly Thr Val Ala Arg Lys Gly Ser Thr Phe Arg Pro 295 300 305	1030
atg gac aca gac act gag gag gtc aga gtg aac act gag gcc agc ggc Met Asp Thr Asp Thr Glu Glu Val Arg Val Asn Thr Glu Ala Ser Gly 310 315 320	1078
cac tat gac tgt cct cac cgc ccg ggc cgc cat gag tac gca ctg cct His Tyr Asp Cys Pro His Arg Pro Gly Arg His Glu Tyr Ala Leu Pro 325 330 335	1126
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ctg ctg cga gct cac acc ttc tcc aca cag agc ggc tac cga gtc cct Leu Leu Arg Ala His Thr Phe Ser Thr Gln Ser Gly Tyr Arg Val Pro 360 365 370	1222
ggg ccc agg ccc act cac aaa cac tcc cat tcc tct gga ggc ttt cct Gly Pro Arg Pro Thr His Lys His Ser His Ser Ser Gly Gly Phe Pro 375 380 385	1270
cct gct aca gga gcc acc cag gtt gaa agc tat cag agg cca gca agc Pro Ala Thr Gly Ala Thr Gln Val Glu Ser Tyr Gln Arg Pro Ala Ser 390 395 400	1318
ccc aag cct gtg ggt ggc tat gac aag cct gct gct agc agc ttc Pro Lys Pro Val Gly Gly Tyr Asp Lys Pro Ala Ala Ser Ser Phe 405 410 415	1366
ttg gac agc aga gac cca gcc tct cag tca cag atg act tcc ggg gga Leu Asp Ser Arg Asp Pro Ala Ser Gln Ser Gln Met Thr Ser Gly Gly 420 425 430 435	1414

gat gat ggt tat tcg gca ccc aga aac ggt ctt gcg ccc ctc aac cag 1462
 Asp Asp Gly Tyr Ser Ala Pro Arg Asn Gly Leu Ala Pro Leu Asn Gln
 440 445 450

acg gcc atg act gct ctt ttg tga acccaatgtg aaagaaacct gctgtggtag 1516
 Thr Ala Met Thr Ala Leu Leu *
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tgagcgcgca ccgctgcgag tcactggaag aatgtgcaa gcgtcatgt gtgactcttc 1576
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 tttttaccgc tttgtctcctt ggaagaaatg aaattacttg aaacatgtaa agcactccag 1996
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 tgaactgggg agttaacctc ttttgc当地 agaggagaaa gtatgtgtc tgtttattga 2656
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 Val Cys Ala Pro Leu Arg Leu Gln Ala Glu Glu Leu Gly Asp Gly Cys
 20 25 30

Gly His Ile Val Thr Ser Gln Asp Ser Gly Thr Met Thr Ser Lys Asn
 35 40 45
 Tyr Pro Gly Thr Tyr Pro Asn Tyr Thr Val Cys Glu Lys Ile Ile Thr
 50 55 60
 Val Pro Lys Gly Lys Arg Leu Ile Leu Arg Leu Gly Asp Leu Asn Ile
 65 70 75 80
 Glu Ser Lys Thr Cys Ala Ser Asp Tyr Leu Leu Phe Ser Ser Ala Thr
 85 90 95
 Asp Gln Tyr Asp Leu Ile Thr Cys Leu Glu Arg Gly Ser His Tyr Phe
 100 105 110
 Glu Glu Lys Tyr Ser Lys Phe Cys Pro Ala Gly Cys Arg Asp Ile Ala
 115 120 125
 Gly Asp Ile Ser Gly Asn Thr Lys Asp Gly Tyr Arg Asp Thr Ser Leu
 130 135 140
 Leu Cys Lys Ala Ala Ile His Ala Gly Ile Ile Thr Asp Glu Leu Gly
 145 150 155 160
 Gly His Ile Asn Leu Leu Gln Ser Lys Gly Ile Ser His Tyr Glu Gly
 165 170 175
 Leu Leu Ala Asn Gly Val Leu Ser Arg His Gly Ser Leu Ser Glu Lys
 180 185 190
 Arg Phe Leu Phe Thr Thr Pro Gly Met Asn Ile Thr Thr Val Ala Ile
 195 200 205
 Pro Ser Val Ile Phe Ile Ala Leu Leu Leu Thr Gly Met Gly Ile Phe
 210 215 220
 Ala Ile Cys Arg Lys Arg Lys Lys Gly Asn Pro Tyr Val Ser Ala
 225 230 235 240
 Asp Ala Gln Lys Thr Gly Cys Trp Lys Gln Ile Lys Tyr Pro Phe Ala
 245 250 255
 Arg His Gln Ser Thr Glu Phe Thr Ile Ser Tyr Asp Asn Glu Lys Glu
 260 265 270
 Met Thr Gln Lys Leu Asp Leu Ile Thr Ser Asp Met Ala Asp Tyr Gln
 275 280 285
 Gln Pro Leu Met Ile Gly Thr Gly Thr Val Ala Arg Lys Gly Ser Thr
 290 295 300
 Phe Arg Pro Met Asp Thr Asp Thr Glu Glu Val Arg Val Asn Thr Glu
 305 310 315 320
 Ala Ser Gly His Tyr Asp Cys Pro His Arg Pro Gly Arg His Glu Tyr
 325 330 335
 Ala Leu Pro Leu Thr His Ser Glu Pro Glu Tyr Ala Thr Pro Ile Val
 340 345 350
 Glu Arg His Leu Leu Arg Ala His Thr Phe Ser Thr Gln Ser Gly Tyr
 355 360 365

Arg Val Pro Gly Pro Arg Pro Thr His His Ser His Ser Ser Gly
370 375 380
Gly Phe Pro Pro Ala Thr Gly Ala Thr Gln Val Glu Ser Tyr Gln Arg
385 390 395 400
Pro Ala Ser Pro Lys Pro Val Gly Gly Tyr Asp Lys Pro Ala Ala
405 410 415
Ser Ser Phe Leu Asp Ser Arg Asp Pro Ala Ser Gln Ser Gln Met Thr
420 425 430
Ser Gly Gly Asp Asp Gly Tyr Ser Ala Pro Arg Asn Gly Leu Ala Pro
435 440 445
Leu Asn Gln Thr Ala Met Thr Ala Leu Leu
450 455

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<220>

<223> peptide tag

<400> 7

Glu Tyr Met Pro Met Glu
1 5

<210> 8

<211> 39

<212> PRT

<213> Artificial Sequence

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<223> polypeptide motif

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<222> (2)...(2)

<223> Xaa is Gly, Ser, Asp or Glu

<221> VARIANT

<222> (3)...(3)

<223> Xaa is Gly, Arg, Tyr, Ser or Thr

<221> VARIANT

<222> (4)...(9)

10003122-114501

<223> Xaa is any amino acid

<221> VARIANT

<222> (10)...(13)

<223> Xaa is any amino acid or not present

<221> VARIANT

<222> (14)...(14)

<223> Xaa is Gly, Ser or Thr

<221> VARIANT

<222> (15)...(15)

<223> Xaa is any amino acid

<221> VARIANT

<222> (16)...(16)

<223> Xaa is Ile, Leu, Phe, Val, Ser or Tyr

<221> VARIANT

<222> (17)...(17)

<223> Xaa is any amino acid

<221> VARIANT

<222> (18)...(18)

<223> Xaa is Ser, Thr, Ala, His or Asn

<221> VARIANT

<222> (19)...(19)

<223> Xaa is Pro, Leu, Ala or Ile

<221> VARIANT

<222> (20)...(20)

<223> Xaa is Asn, Ser, Glu, Asp or His

<221> VARIANT

<222> (21)...(21)

<223> Xaa is Tyr, Phe, Trp and Gly

<221> VARIANT

<222> (22)...(22)

<223> Xaa is Pro, Ile or Gly

<221> VARIANT

10001324150501

<222> (23) . . . (23)

<223> Xaa is any amino acid

<221> VARIANT

<222> (24)...(24)

<223> Xaa is any amino acid

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<223> Xaa is any amino acid or not present

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<222> (27)...(27)

<223> Xaa is any amino acid or not present

<221> VARIANT

<222> (28)...(28)

<223> Xaa is Tyr, Phe, Ser or Asp

<221> VARIANT

<222> (29)...(29)

<223> Xaa is any amino acid

<221> VARIANT

<222> (30)...(30)

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<222> (32)...(32)

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<221> VARIANT

<222> (33)...(33)

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<221> VARIANT

<222> (34)...(34)

<223> Xaa is any amino acid or not present

<221> VARIANT

<222> (36)...(36)

<223> Xaa is any amino acid

<221> VARIANT

<222> (37)...(37)

<223> Xaa is Trp, Tyr, Lys or Arg

<221> VARIANT

<222> (38)...(38)

<223> Xaa is any amino acid

<221> VARIANT

<222> (39)...(39)

<223> Xaa is Ile, Leu, Val or Phe

<400> 8

Cys Xaa Xaa

1

5

10

15

Xaa Xaa

20

25

30

Xaa Xaa Cys Xaa Xaa Xaa Xaa

35

<210> 9

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<213> Artificial Sequence

<220>

<223> polypeptide motif

<221> VARIANT

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<223> Xaa is Lys, Arg, Gly, Ala, Ile, Leu, Trp or Pro

<221> VARIANT

<222> (3)...(3)

<223> Xaa is Tyr, Trp, Lys, Ile or Ser

<221> VARIANT

<222> (4)...(4)

<223> Xaa is Asp or Glu

<221> VARIANT

<222> (5)...(5)

<223> Xaa is Trp, Tyr, Phe, Gln, Ser, Ala, Val or Ile

<221> VARIANT

<222> (6)...(16)

<223> Xaa is any amino acid

<221> VARIANT

<222> (17)...(20)

<223> Xaa is any amino acid or not present

<221> VARIANT

<222> (21)...(21)

<223> Xaa is Gly, Asn, Glu or Met

<221> VARIANT

<222> (22)...(22)

<223> Xaa is Lys, Arg, Ile, Val, Ser or Pro

<221> VARIANT

<222> (23)...(23)

<223> Xaa is Trp, Tyr, Phe, Leu, Ile or Met

<400> 9

Cys Xaa Xaa

1

5

10

15

Xaa Xaa Xaa Xaa Xaa Xaa Cys Gly

20

25

<210> 10

<211> 36

<212> PRT

<213> Artificial Sequence

<220>

<223> polypeptide motif

10003122-141501

<221> VARIANT
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<223> Xaa is Gly, Ala or Ser

<221> VARIANT
<222> (3)...(9)
<223> Xaa is any amino acid

<221> VARIANT
<222> (10)...(17)
<223> Xaa is any amino acid or not present

<221> VARIANT
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<223> Xaa is Phe, Tyr or Trp

<221> VARIANT
<222> (19)...(19)
<223> Xaa is Leu, Ile or Val

<221> VARIANT
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<223> Xaa is Leu, Ile, Val, Phe or Ala

<221> VARIANT
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<223> Xaa is Gly, Ser, Thr, Asp, Glu or Asn

<221> VARIANT
<222> (23)...(28)
<223> Xaa is any amino acid

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<223> Xaa is Leu, Ile, Val or Phe

<221> VARIANT
<222> (30)...(31)
<223> Xaa is any amino acid.

<221> VARIANT
<222> (32)...(32)
<223> Xaa is Ile or Val

<221> VARIANT
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<223> Xaa is any amino acid

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<222> (34)...(34)
<223> Xaa is Lys, Ile, Val or Thr

<221> VARIANT
<222> (35)...(35)
<223> Xaa is Gln, Lys or Met

<400> 10
Xaa Trp Xaa
1 5 10 15
Xaa
20 25 30
Xaa Xaa Xaa Gly
35

<210> 11
<211> 19
<212> PRT
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<220>
<223> polypeptide motif

<221> VARIANT
<222> (2)...(9)
<223> Xaa is any amino acid

<221> VARIANT
<222> (10)...(11)
<223> Xaa is any amino acid or not present

<221> VARIANT
<222> (12)...(12)

10003132-1155

<223> Xaa is Leu or Met

<221> VARIANT

<222> (14)...(14)

<223> Xaa is any amino acid

<221> VARIANT

<222> (15)...(15)

<223> Xaa is Gly or Glu

<221> VARIANT

<222> (16)...(16)

<223> Xaa is Leu, Ile, Val or Pro

<221> VARIANT

<222> (17)...(17)

<223> Xaa is any amino acid

<400> 11

Pro	Xaa	Arg	Xaa	Xaa	Xaa									
1														
												10		15
Xaa	Gly	Cys												

<210> 12

<211> 2145

<212> DNA

<213> Artificial Sequence

<220>

<223> degenerate nucleotide sequence

<221> misc_feature

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<223> n = A,T,C or G

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gcnytntny	tngcngtnws	ngcnccnytn	mgnytncarg	cngargaryst	ngngayggn	120
tgyggncayy	tngtnacnta	ycargaywsn	ggnacnatga	cnwsnaaraa	ytagccngn	180
acntayccna	aycayacngt	ntgygaraar	acnathacng	tnccnaargg	naarmgnytn	240
athytnmgny	tnggngayyt	ngayathgar	wsncaracnt	gygcnwsgna	ytagytnytn	300
ttyacnwsnw	snwsngayca	rtayggncn	taytgyggnw	snatgacngt	nccnaargar	360

<210> 13

<211> 1509

<212> DNA

<213> Artificial Sequence

<220>

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<221> misc feature

<222> (1) (1509)

<223> n = A T C or G

<400> 13

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ytnmgnytnc argcngarga rytnngngay ggntgyggnc ayathgtiac nwsncargay 120
wsnggnacna tgacnwsnaa raaytayccn ggnacntayc cnaaytayac ngtnagygar 180
aarathatha cngtnccnaa rggnaarmgn ytnathytnm gnytnngngya yytnaayath 240
garwsnaara cntgygcnw sngcnaacng ycartayggncntaytgyg gnwsntggcngtncnaar garytnmgny tnaaywsnaa ygargtnacn 300
gtnytnyya arwsnggnws ncayathwsn ggnmgngnt tyytnytnac ntaygcnwsn 360
wsngaycayc cngayytnat hacntgyytn garmgnggnw sncaytaytt ygargaraar 420
taywsnaart tytgycnngc ngntgymgn gayathgcng gngayathws ngnaayacn 480
aargayggnt aymngayac nwsnytnytn tgyaargcng cnathcaygc nggnathath 540
acngaygary tnngngnca yathaayytn ytncarwsna arggnathws ncaytaygar 600
ggnytnytnng cnaayggngt nytnwsnmgn cayggwnsny tnwsngaraa rmgnattytn 660
ttyacnacnc. cnggnatgaa yathacnacn gtngcnathc cnwsngtnat httyathgcn 720
tynytynyna cnggnatgg nathtygcn athtgymgn armgnaraa raarggnaya 780
ccntaygtnw sngcngaygc ncaraaracn ggntgytgga arcaraatha rtayccnny 840
gcnmgncayc arwsnacnga rttyacnath wsntaygaya aygaraarga ratgacncar 900
aarytngayy tnathacnws ngayatggc gaytaycarc arccnytnat gathggna 960
gnacngtng cnmgnaargg nwsnacntt mgnccnatgg ayacngayac ngargargtn 1020
mngtynaaya cngargcnws ngncaytay gaytgyccnc aymgnccngg nmgnccaygar 1080
taygcnytnc cnytnacnca ywsngarccn gartaygcna cnccnathgt ngarmgnccay 1140
ytnytnmgng cncayacntt ywsnacncar wsnggntaym gngtncnngg nccnmgncn 1200
acncayaarc aywsncayws nwsngnggn ttcnccng cnacnggngc nacncargtn 1260
garwsntayc armgnccngc nwsnccnaar ccngtngng gnggntayga yaarcncn 1320
gcnwsnwsnt tyytngayws nmngayccn gcnwsncarw sncaratgac nwsngnggn 1380
gaygagggnt aywsngcncc nmgnaygn ytnytnccny tnaaycarac ngcnatgacn 1440
gcnaytynyn 1500
1509

<210> 14

<211> 1374

<212> DNA

<213> Artificial Sequence

<220>

<223> degenerate nucleotide sequence

<221> misc feature

<222> (1) . . . (1374)

<223> n = A,T,C or G

<400> 14

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ytnmgnytnc argcngarga rytnngngay ggntgyggnc ayathgtnc nwsncargay 120

FOURTY-SEVEN

wsnggnacna tgacnwsnaa raaytayccn ggnacntayc cnaaytayac ngtntgygar	180
aarathatha cngtnccnaa rggnaarmgn ytnathytnm gnytnngnga yttnaayath	240
garwsnaara cntgygcnws ngaytayytн ytnattywsnw sngcnacnga ycartaygay	300
ytnathacnt gyytngarmg nggnwsncay tayttygarg araartayws naarttytgy	360
ccngcngngt gymgngayat hgcnngngay athwsngna ayacnaarga yggntaymgn	420
gayacnwsny tnytntgyaa rgcngcnath caygcngna thathacnga ygarytnngn	480
ggncayatha ayytynytcnа rwsnaarggn athwsncayt aygarggnyt nytnacnay	540
ggngtnytnw snmgncaygg nwsnytnwsn garaarmgn tyytnattyac nacnccngn	600
atgaayatha cnacngtngc nathccnwsn gtnathetta thgcnytnyt nytnacnngn	660
atgggnatht tygcnathtg ymgnaarmgn aaraaraarg gnaayccnta ygtwnsngcn	720
gaygcncara aracnggntg ytggAACar car ahaartayc cnytgcnmg ncaycarwsn	780
acngarttya cnathwsnta ygayaaygar aargaratga cncaraaryt ngayytnath	840
acnwsngaya tggcngayta ycarrccn ytnatgathg gnacnggnac ngtnngcnmgn	900
aarggnwsna cnytymgncc natggayacn gayacngarg argtnmngt naayacngar	960
gcnwsngngc aytaygaytg yccncaymgn ccnggnmgnc aygartaygc nytnccnytn	1020
acncaywsng arccngarta ygcnaecnccn athgtngarm gnccaytnty nmngncncay	1080
acnytysna cncarwsngg ntaymngn tccngnccnm gnccnaecnca yaarcaywsn	1140
caywsnwsgn gnggnttycc nccngcnacn ggngcnacnc argtngarws ntaycarmgn	1200
ccngcnwsnc cnaarccngt ngngngngn taygayaarc cngcngcnws nwsnttyn	1260
gaywsnmng aycngcnws ncarwsncar atgacnwsng gngngayga yggntaywsn	1320
gcnccnmgn aygnytngc nccnytnaay caracngcna tgacngcnyt nytn	1374

<210> 15

<211> 1001

<212> DNA

<213> Homo sapiens

<400> 15

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